AMENDMENT TO THE CLAIMS

Please amend the claims as follows.

1. (Currently Amended) A method for performing expression proteomic analysis, comprising:

inducing a subtle isotope modification in an organism or sample;

analyzing said subtle isotope modification with an analytic tool; and

performing expression proteomic analysis on the organism or sample with the analysis of said subtle isotope modification.

2. (Original) The method of claim 1 wherein said analytic tool is used to monitor turnover of peptides, polypeptides or both.

3. (Original) The method of claim 1 wherein said analytic tool is configured to calculate an isotope ratio for specific peptides or polypeptides by measuring isotope distributions.

4. (Original) The method of claim 1 wherein said organism is a mammal.

5. (Original) The method of claim 1 wherein said organism is a human.

6. (Original) The method of claim 1 wherein said subtle isotope modification includes swapping of ^{13}C for ^{12}C, ^{18}O for ^{16}O, ^{15}N for ^{14}N, deuterium for hydrogen, or combinations thereof.

7. (Currently Amended) The method of claim 1 wherein said subtle isotope ratio modification results in a modification of a ~~$^{13}C:^{12}C$~~ $^{12}C:^{13}C$ isotope ratio of from about 100:1 to about ~~200:1~~ 100:2.

8. (Original) The method of claim 1 wherein said subtle isotope modification is induced by a method selected from the group consisting of isotope-coded affinity tag (ICAT), stable isotope labeling with amino acids in cell culture (SILAC), enzymatic exchange, growth in stable isotopes, diet, injection and combinations thereof.

9. (Original) The method of claim 1 wherein said subtle isotope modification is analyzed by a method selected from the group consisting of matrix-assisted laser desorption ionization time-of-flight (MALDI-TOF) mass spectrometry, micro-liquid chromatography with tandem mass spectrometry (LC-MSMS), high resolution mass spectrometry, tandem mass spectrometry (MSMS), Fournier transform mass spectrometry (FTMS), averagine, isotope ratio mass spectrometry (IRMS) and combinations thereof.

10. (Currently Amended) A system for analyzing isotope distribution, comprising:

an organism in which a subtle isotope modification has been induced to perform expression proteomic analysis on the organism; and

an analytic tool to analyze said subtle isotope modification configured to analyze turnover of peptides, polypeptides or both.

Claim 11 (Canceled).

12. (Original) The system of claim 10 wherein said analytic tool is configured to calculate an isotope ratio for specific peptides or polypeptides by measuring isotope distributions.

13. (Original) The system of claim 10 wherein said organism is a mammal.

14. (Original) The system of claim 10 wherein said organism is a human.

15. (Original) The system of claim 10 wherein said subtle isotope modification includes swapping of ^{13}C for ^{12}C, ^{18}O for ^{16}O, ^{15}N for ^{14}N, deuterium for hydrogen, or combinations thereof.

16. (Currently Amended) The system of claim 10 wherein said subtle isotope ratio modification results in a modification of a ~~$^{13}C:^{12}C$~~ $^{12}C:^{13}C$ isotope ratio of from about 100:1 to about ~~200:1~~ 100:2.

17. (Original) The system of claim 10 wherein said subtle isotope modification is induced by a method selected from the group consisting of isotope-coded affinity tag (ICAT), stable isotope labeling with amino acids in cell culture (SILAC), enzymatic exchange, growth in stable isotopes, diet, injection and combinations thereof.

18. (Original) The system of claim 10 wherein said analytic tool is configured to analyze said subtle isotope modification by a method selected from the group consisting of matrix-assisted laser desorption ionization time-of-flight (MALDI-TOF) mass spectrometry, micro-liquid chromatography with tandem mass spectrometry (LC-MSMS), high resolution mass spectrometry, tandem mass spectrometry (MSMS), Fournier transform mass spectrometry (FTMS), averagine, isotope ratio mass spectrometry (IRMS) and combinations thereof.

19. (Original) A method for performing expression proteomic analysis, comprising:

providing an elemental composition in which a subtle isotope modification has been induced;

analyzing said subtle isotope modification with the Isosolv algorithm.

20. (Original) The method of claim 19 wherein said subtle isotope modification includes swapping of ^{13}C for ^{12}C, ^{18}O for ^{16}O, ^{15}N for ^{14}N, deuterium for hydrogen, or combinations thereof.

21. (Currently Amended) The method of claim 19 wherein said subtle isotope ratio modification results in a modification of a ~~$^{13}C:^{12}C$~~ $^{12}C:^{13}C$ isotope ratio of from about 100:1 to about ~~200:1~~ 100:2.

22. (Original) The method of claim 19 wherein said subtle isotope modification is induced by a method selected from the group consisting of isotope-coded affinity tag (ICAT), stable isotope labeling with amino acids in cell culture (SILAC), enzymatic exchange, growth in stable isotopes, diet, injection and combinations thereof.

23. (Original) The method of claim 19 wherein said subtle isotope modification is analyzed by a method selected from the group consisting of matrix-assisted laser desorption ionization time-of-flight (MALDI-TOF) mass spectrometry, micro-liquid chromatography with tandem mass spectrometry (LC-MSMS), high resolution mass spectrometry, tandem mass spectrometry (MSMS), Fourier transform mass spectrometry (FTMS), averagine, isotope ratio mass spectrometry (IRMS) and combinations thereof.